RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/830, 837B

Source: 1F~/6

Date Processed by STIC: 2/23/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _09/830,837ß_ CRF Edit Date: _2/23/06_
Edited by: _hw_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_✓_ Corrected the SEQ ID NO. Sequence numbers edited were:

_6/,87_

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_✓_ Deleted: _✓_ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

Revised 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 02/24/2006
PATENT APPLICATION: US/09/830,837B   TIME: 15:45:00

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02242006\I830837B.raw

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 3 <110> APPLICANT: Institut de Recherches Cliniques de Montreal
 4        Seidah, Nabil
 5        ChrEtien, Michel
 6        Marcinkiewicz, Mieczyslaw
 7        Laaksonen, Reijo
 8        Davignon, Jean
10 <120> TITLE OF INVENTION: MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
CONVERTASE
11        WITH A UNIQUE CLEAVAGE SPECIFICITY
13 <130> FILE REFERENCE: 10992.29
15 <140> CURRENT APPLICATION NUMBER: US 09/830,837B
16 <141> CURRENT FILING DATE: 2001-10-18
18 <150> PRIOR APPLICATION NUMBER: PCT/CA1999/01058
19 <151> PRIOR FILING DATE: 1999-11-04
21 <150> PRIOR APPLICATION NUMBER: CA 2,249,648
22 <151> PRIOR FILING DATE: 1998-11-04
24 <160> NUMBER OF SEQ ID NOS: 108
26 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 3895
30 <212> TYPE: DNA
31 <213> ORGANISM: Rattus sp.
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36 <222> LOCATION: (418)..(3573)
38 <400> SEQUENCE: 1
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43 tcctgctaga tttgggtctg tggtacaaat ggagtttagg actcagtgga ctcggcccta     180
45 atgagagaag cccccctgtcc aagatggaga agaagcggag aaagaaatga aagcctcttt     240
47 ttgggccaag ctgtgggtga ccatgggact gaggttttct ttacgttgga caagtctgta     300
49 ggatggctga tcagtaaggt tgcagctttt agcgaaaaca gaaatccact tctgatcaag     360
51 gaagagccta gtgcaatttg aatttatgca attttatgac catattcact taggacc       417
53 atg aag ctc gtc aac atc tgg ctt ctt ctg ctg gtg gtt ttg ctc tgt      465
54 Met Lys Leu Val Asn Ile Trp Leu Leu Leu Leu Val Val Leu Leu Cys
55 1               5                   10                  15
57 ggg aaa aag cat ctg ggt gac agg ctg ggg aag aaa gct ttt gaa aag      513
58 Gly Lys Lys His Leu Gly Asp Arg Leu Gly Lys Lys Ala Phe Glu Lys
59             20                  25                  30
61 gcc cca tgc ccc agc tgt tcc cac ctg act ttg aag gtg gaa ttc tcc      561
62 Ala Pro Cys Pro Ser Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser
63             35                  40                  45
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66 Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
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70 Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
71 65                    70                    75                    80
73 gaa gtg gac aac tgg aga ata ata cct cgg aac aac cca tct agt gac        705
74 Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
75                    85                    90                    95
77 tac cct agt gat ttt gag gtg att cag ata aaa gag aag cag aag gcg        753
78 Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
79              100                   105                   110
81 ggg ctg ctc aca ctt gaa gat cac cca aac atc aag cgg gtg aca ccc        801
82 Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
83         115                   120                   125
85 cag cgg aaa gtc ttt cgt tcc ctg aag ttt gct gaa tcc gac ccc att        849
86 Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asp Pro Ile
87         130                   135                   140
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91 145                   150                   155                   160
93 ccc ctg aaa aga gcc agt ctc tcc ctg ggc tct gga ttc tgg cat gca        945
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95                   165                   170                   175
97 aca gga agg cat tca agt cga cga ttg ctg aga gcc att cct cgc cag        993
98 Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
99              180                   185                   190
101 gtt gcc cag aca ttg cag gca gat gtg ctt tgg cag atg gga tac aca      1041
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103         195                   200                   205
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107         210                   215                   220
109 cat cca cat ttc aag aat gtg aag gaa aga acc aac tgg acc aat gag      1137
110 His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
111 225                   230                   235                   240
113 cgg acc ctg gac gat ggg ctg ggc cat ggc aca ttc gtt gca ggt gtg      1185
114 Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
115              245                   250                   255
119 att gcc agc atg aga gag tgc caa gga ttt gcc cca gat gca gag ctg      1233
120 Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
121         260                   265                   270
123 cac atc ttc agg gtc ttt acc aac aat cag gtg tct tac acg tct tgg      1281
124 His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
125         275                   280                   285
127 ttt ttg gat gcc ttc aac tat gcc atc cta aag aag atg gac gtt ctg      1329
128 Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu
129         290                   295                   300
131 aac ctt agc atc ggt ggg cct gac ttc atg gat cac ccc ttt gtt gac      1377
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139 ggc aat gat gga cct ctc tat ggc act ctg aat aac cct gct gat cag    · 1473
140 Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln
141             340                 345                 350
143 atg gat gtg att gga gtg ggt ggc att gac ttt gaa gac aac atc gcc      1521
144 Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala
145             355                 360                 365
147 cgc ttc tct tcc agg gga atg act acc tgg gaa cta ccg gga ggc tat      1569
148 Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr
149     370                 375                 380
151 ggt cgt gtg aag cct gac att gtc acc tat ggt gct gga gtg cgg ggt      1617
152 Gly Arg Val Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly
153 385                 390                 395                 400
155 tct ggt gtg aaa ggg ggc tgc cgt gca ctc tca ggg acc agt gtc gcc      1665
156 Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala
157             405                 410                 415
159 tcc cca gtg gtt gct ggg gct gtc acc ttg tta gta agc aca gta cag      1713
160 Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln
161             420                 425                 430
163 aag cgg gag cta gtg aat cct gcc agt gtg aag caa gct ttg ata gca      1761
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165             435                 440                 445
167 tca gcc cgg aga ctt cct ggt gtc aac atg ttt gag caa ggc cat ggc      1809
168 Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly
169     450                 455                 460
171 aag ttg gat cta ctg cga gcc tat cag atc ctc agc agc tat aaa ccg      1857
172 Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Ser Ser Tyr Lys Pro
173 465                 470                 475                 480
175 cag gcg agc ctg agt cct agc tac atc gac ctg act gag tgt ccc tac      1905
176 Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr
177             485                 490                 495
179 atg tgg ccc tac tgc tcc cag ccc atc tac tat gga gga atg cca aca      1953
180 Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr
181             500                 505                 510
183 att gtt aat gtc acc atc ctc aat ggc atg gga gtt aca gga aga att      2001
184 Ile Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile
185             515                 520                 525
187 gtg gat aag cct gag tgg cga ccc tat tta cca cag aat gga gac aac      2049
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192 Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly
193 545                 550                 555                 560
195 tac ctt gcc atc tcc att tct gtg acc aag aag gca gct tcc tgg gaa      2145
196 Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu
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204 Thr Glu Leu Lys Asn Gly Ala Glu His Thr Ser Thr Val Lys Leu Pro
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207 atc aag gtg aag atc att ccc acc cct cct cgg agc aag aga gtc ctc   2289
208 Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu
209         610                 615                 620
211 tgg gac cag tac cac aac ctc cgc tac cca ccc ggc tac ttc ccc agg   2337
212 Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg
213 625                 630                 635                 640
215 gac aac ttg cgg atg aag aat gat cct tta gac tgg aat ggc gac cac   2385
216 Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His
217             645                 650                 655
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224 Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys Phe Asp Ala Thr
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229         690                 695                 700
231 gag gag att gct aag ctg agg agg gac gtg gac aat ggc ctt tcc ctt   2577
232 Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu Ser Leu
233 705                 710                 715                 720
237 gtc gtc ttc agt gac tgg tac aac act tct gtt atg aga aaa gtg aag   2625
238 Val Val Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys
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241 ttt tac gat gaa aac aca agg cag tgg tgg atg cca gat act gga gga   2673
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243             740                 745                 750
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246 Ala Asn Val Pro Ala Leu Asn Glu Leu Leu Ser Val Trp Asn Met Gly
247         755                 760                 765
249 ttc agt gac ggc ctg tat gaa ggg gag ttt gcc ctg gca aac cac gac   2769
250 Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Ala Leu Ala Asn His Asp
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253 atg tac tat gca tcg ggg tgc agc att gcc agg ttt cca gaa gat ggt   2817
254 Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Arg Phe Pro Glu Asp Gly
255 785                 790                 795                 800
257 gtg gtg atc aca cag act ttc aag gac caa gga ttg gaa gtc tta aaa   2865
258 Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu Glu Val Leu Lys
259             805                 810                 815
261 caa gag aca gca gtt gtc gac aat gtc ccc att ctg ggg cta tat cag   2913
262 Gln Glu Thr Ala Val Val Asp Asn Val Pro Ile Leu Gly Leu Tyr Gln
263             820                 825                 830
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271     850              855              860
273 gca ctc ctt cag tac aca tcc tat ggt gtg acc cct ccc agc ctc agc    3057
274 Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser
275 865              870              875              880
277 cat tca ggg aac cgg cag cgc cca ccc agc ggg gct ggc ttg gcc cct    3105
278 His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Leu Ala Pro
279              885              890              895
281 cct gaa agg atg gaa gga aac cac ctt cat cgc tac tcc aaa gtt ctt    3153
282 Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
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285 gag gcc cac ttg gga gac ccg aaa cct cgg ccc ctt cca gcc tgt cca    3201
286 Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
287     915              920              925
289 cac ttg tcg tgg gcc aag cca cag cct ttg aat gag acg gca ccc agt   .3249
290 His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
291     930              935              940
293 aat ctt tgg aaa cac cag aag ctg ctc tcc att gac ctg gac aaa gta    3297
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295 945              950              955              960
297 gtg tta ccc aac ttt cgc tca aat cgc cct caa gtg aga cct ttg tcc    3345
298 Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
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301 cct gga gaa agt ggt gcc tgg gac att cct gga ggg atc atg cct ggc    3393
302 Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
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305 cgc tac aac cag gaa gta ggc cag  acc atc cct gtt ttt  gcc ttc ctt  3441
306 Arg Tyr Asn Gln Glu Val Gly Gln  Thr Ile Pro Val Phe  Ala Phe Leu
307         995              1000              1005
309 gga gcc  atg gtg gcc ctg gcc  ttc ttc gtg gta cag  atc agt aag     3486
310 Gly Ala  Met Val Ala Leu Ala  Phe Phe Val Val Gln  Ile Ser Lys
311     1010              1015              1020
313 gcc aag  agc cgg ccg aag cgg  agg agg ccc agg gca  aag cgt cca     3531
314 Ala Lys  Ser Arg Pro Lys Arg  Arg Arg Pro Arg Ala  Lys Arg Pro
315     1025              1030              1035
317 caa ctt  gca cag cag gcc cac  cct gca agg acc ccg  tca gtg         3573
318 Gln Leu  Ala Gln Gln Ala His  Pro Ala Arg Thr Pro  Ser Val
319     1040              1045              1050
321 tgatcatcac agtggccaga cacagaagct gacaagcttt gaacccctct ggtggccaca   3633
323 cagcatcaga gagcatcctg ggaagtgcct gtttccaagg agccctatct ctggattgtg   3693
325 gctggcttag tgtgttctgc ccagacgtct atgaggtaca tcctgcagtg cctcactgtg   3753
327 tttggctctg gccgaaggtg cccagtagct cagcctccgg tggcatcagg cccagtgaca   3813
329 gtgcaccaaa gacacagagc ctggaagggc tgtcgggaca tactttctac ataatgctac   3873
331 aaccctgacc aagcgaagac at                                           3895
334 <210> SEQ ID NO: 2
335 <211> LENGTH: 1052
336 <212> TYPE: PRT
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/24/2006
PATENT APPLICATION: US/09/830,837B   TIME: 15:45:01

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02242006\I830837B.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:8; Xaa Pos. 2,3,4,5,6,7
Seq#:9; Xaa Pos. 2,3,4,5,6,7,8
Seq#:10; Xaa Pos. 2,3,4,5,6,7,8
Seq#:11; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:12; Xaa Pos. 2,3,4,5,6,7,8,9
Seq#:14; Xaa Pos. 1,13
Seq#:15; N Pos. 3,9,12,18,21
Seq#:16; N Pos. 3,6,9,12,15,18,21,24,29
Seq#:17; Xaa Pos. 5,6
Seq#:18; Xaa Pos. 4,6,8,10
Seq#:46; Xaa Pos. 1,13
Seq#:47; Xaa Pos. 1,11
Seq#:74; Xaa Pos. 1,13
Seq#:75; Xaa Pos. 1,11
Seq#:76; Xaa Pos. 1,14
Seq#:101; Xaa Pos. 1
Seq#:102; Xaa Pos. 1
Seq#:103; Xaa Pos. 6
Seq#:107; Xaa Pos. 1,11

VERIFICATION SUMMARY   DATE: 02/24/2006
PATENT APPLICATION: **US/09/830,837B**   TIME: 15:45:01

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\02242006\I830837B.raw**

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:1852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:2005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
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Raw Sequence Listing before editing (for reference only)

IFW16

RAW SEQUENCE LISTING   DATE: 02/23/2006
PATENT APPLICATION: US/09/830,837B   TIME: 11:44:13

Input Set : A:\PTO.TS.23.txt
Output Set: N:\CRF4\02232006\I830837B.raw

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   3 <110> APPLICANT: Institut de Recherches Cliniques de Montreal
   4         Seidah, Nabil
   5         ChrEtien, Michel
   6         Marcinkiewicz, Mieczyslaw
   7         Laaksonen, Reijo
   8         Davignon, Jean
  10 <120> TITLE OF INVENTION: MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN
CONVERTASE
  11         WITH A UNIQUE CLEAVAGE SPECIFICITY
  13 <130> FILE REFERENCE: 10992.29
  15 <140> CURRENT APPLICATION NUMBER: US 09/830,837B
C--> 16 <141> CURRENT FILING DATE: 2001-10-18
  18 <150> PRIOR APPLICATION NUMBER: PCT/CA1999/01058
  19 <151> PRIOR FILING DATE: 1999-11-04
  21 <150> PRIOR APPLICATION NUMBER: CA 2,249,648
  22 <151> PRIOR FILING DATE: 1998-11-04
  24 <160> NUMBER OF SEQ ID NOS: 108
  26 <170> SOFTWARE: PatentIn version 3.3
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Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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     2759 <212> TYPE: PRT
     2760 <213> ORGANISM: Bovis sp.
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RAW SEQUENCE LISTING   DATE: 02/23/2006
PATENT APPLICATION: US/09/830,837B   TIME: 11:44:13

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Output Set: N:\CRF4\02232006\I830837B.raw

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     3396 1/34

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:1852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:1887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:1965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:2005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:2033 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:2038 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:2044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:2083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:2141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:2165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:2201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:2585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:2610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0
L:2757 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 61 thru 63
L:2762 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:64 differs:61
L:2768 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 62
L:2928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
L:2953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0
L:2978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
L:3105 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:87 differs:78
L:3279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:0
L:3299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102 after pos.:0
L:3319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0
L:3377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:107 after pos.:0
L:3393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:108